

Figure 1

YNGWEDPWGQGTLVTVSS (SEQ ID NO:1)
CDR3

Figure 2

VSGGSINsgD~~YXW~~SWRQH~~E~~GKglDCguyxsgslylins
CDR1 CDR2

GGAT TGGGTACATCTTACAGTG GGAGCCACTA
GAGGCC GGTATTACT

vsggsiNsgDxxwsrwrohfgkglDCgixysgsll
CDR1 CDR2

Figure 2

AGCACCTA
GTTTACTT

GTCTCTGTC GTCATCAA CAGGGTGTACTA GCTGACCTCG
 AGATCAGTCTTGCTGAAGCTGACCTCG TGTACGCTG
 (SEQ ID NO:1) ③
 CTACAAACCCG TCCCTCAAGA GTCGAGTTAC CATACTACTA
 GACACGCTTA AGAATCAGTCTTGCTGAAGCTGACCTCG
 CTACAAACCCG TCCCTCAAGA GTCGAGTTAC CATACTACTA
 GACACGCTTA AGAATCAGTCTTGCTGAAGCTGACCTCG
 GTGGGAGATCTACGGGTGTA ATCCGGGGT GGTCACGCC
 GTGGGAGATCTACGGGTGTA ATCCGGGGT GGTCACGCC

(SEQ ID NO: 4) 

CDR2

ATTING

TRICOASOBA
CDR 1

102

TGICAA

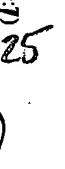
Figure 4

三

ACCATCACTT GCCAGGGGAG TCGAGGACATT AAC
GAAACAGGGG GCCCCATCAAG GTTCAGTGGA AG
CAGTATGAAA GTCTC CCACTCACTT TCGGGGGAA

TGICAA

Figure 5

vsggsiNsgDDYxwswirohpGkglewigSiyysgNtFyneslksrvtsldisknoseklssvtadavCycarnivtigaedjwgqqtmtvss (SEQ ID NO:7) 

CDR1

CDR2

CDR3

gtctctggtg gctccatcaa cagtcgttat tactactgga gctggatccc ccagcacca gggaggcc tggagtggat tggccatc tattacagtggAACACCCIT
ctacaaccggcccccraaga gtcgagttac catatca GACAGCTA AGAACCGT CTCCTGAQ CTGAGTTG TGACTGCCG GGACACGGCC GTGTGTACT
gtcgagaaa TATAGTGACT ACGGGTGTT TIGATACTG GGGCAAGGG ACAATGGCA CGCTCTCA (SEQ ID NO:8) 

Figure 6

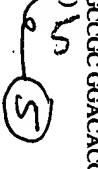
ttcoasoditIlylnwyiookpgkapkllindassletgvpvlrfsgsgstdef*misslopediatyxcqoyd*Hupljfcgctkvakrtv/aapsvfifpsdEQ (SEQ ID NO:9) 

CDR1

CDR2

CDR3

Figure 7

accatcaatt gtcaggcag tcagacatt accattattaaatgtta tcaacagaa ccaggaaag ccctt aagctctgttcaacggcgc atccagttt
gaaacagggg tcccattaag gttcagtggaa agtggatctggatctttacttttcaccatctag cagctgcag ctgtcaaa tgcaacata ttacctgtcaaa
cgtatgtatca tccgtcaactt tccgggggg gaccaagggtt gggatcaa (SEQ ID NO:10) 



(SEQ ID NO:9) 

(SEQ ID NO:9) 

Figure 8

Figure 9

vsggsissgDYwTirrohgkglewgyxxsgNTyxneslksrvSMsIdsEnofSLKLSVTAdtavycarkepvgedxwgqgtlvtvs (SEQ ID NO: 14)

CDR1

CDR2

CDR3

43

GTCTCTGGTG GTCRCCATCAG CAGTGTGAT TACTACTGGA CCTGGATCCG CCAGCACCA GCGAAGGCC TGGAGTGGAT TGGGACATC TATTACAGTG GGAACACCTA
CTACAACCCG TCCTCTCAAGA GTCGAGTTTC CATGTCATA GACACGCTG AGAACCGAGT CTGAGCTCTG TOACTGGCCG GCAACACGGCC GTGTATTACT
GTCGGAGAA ACCAGTGTACT GGCGGGAGG ACTACTGGG CCAGGAACTCCTGGTCACCCG TCTCTCTA (SEQ ID NO: 15)

7

Figure 10

ttccQASODISNYNWYOKPGKAPKLIVDASNETGVRSRSGSGIDFTISLOPEDIYGYYQOESLPCGFQGTKLEIRTVAAPSVFIPSDQ (SEQ ID NO: 16)

CDR1

CDR2

CDR3

44

Figure 11

ACCATCACTT GCGAGGCAG TCAGGACATT AGTAACATT TAATGTA TCAGGAGAA CCAGGGAAAG CCCT AAGCTCTGA TCTACCGATGC TICCAATTG GAAACAGGG
TCCCATCAAG GTCAGTGGA GTCGATCTG GGACA GATTACTT TCACCATCAG CAGCCTGCAG CCTGAAGATG TICGAACATA TGTCTGCAA CAGTATGAGA GTCCTC
CCGTGGGGTT TGGCAGGG GACCAAACCTGGAGATCAA (SEQ ID NO: 17)

44

Figure 12

Figure 13

VSGGSINsgD**F**ywswRohrgkglewigYXxgSIVToneSksrvtMsIdPsknosiLsVtaadIavtycaT**I**slYyggMDywgQGRTVSS (SEQ ID NO:16)

CDR1

CDR2

CDR3

Figure 14

GTCCTGGTG GTCGCCATCAA CAGTGTTGAT TTCTACTGGGA GCTGGATCCG CCAACACCCA GGAAAGGGCC TGGAGTGGAT TGGGTACATC TATTACAGTG GGAGCACCTA
CTACAACCCG TCCCTCAAGA GTCCGAGTTAC CATGTCATA GACCGCTTA AGAACCCAGT CTCCCTGAA CTGATCTG TGACTGCCC GGACACGGCC GTTATTACT
GTGGGACNTC CCTTACTAT GGCGGGGTA TGGACGCTG GGGCCAAGGG ACCACGGTCA CGTCTCCCA (SEQ ID NO:16)

⑨

Figure 15

TITCQASODISNNLNWYOOKRGNAPKLLIVDASNLIEGYPSRSQSGSGIDFTFISNLOPEDIATYCYQHMDPLPWTFCQIKVEXKRTVAAPSVFIFPPSDEQ (SEQ ID NO:17)

CDR1

CDR2

CDR3

⑩

Figure 16

ACCATCACTT GCCAGGGGAG TCAGGACATT AACAACTATT TGAATGGTA TCAGCAGAGG CCNGGAACG CCGCTTAAACTCTGA TCTACGATGC ATCCAAATTG
GAAACAGGGG TCCCATCAA GTTCAGTGGAA AGTGGATCTG GGACA GATTTACTT TCACCATCAA CAGCTCCAG CCTGAAGATA TTCCACATA TTATGCAA
(SEQ ID NO:18)

⑪

⑫

Figure 17

VS~~GGSINN~~D~~YX~~WSWIROH~~P~~GLEW~~G~~H~~U~~S~~G~~STY~~U~~FS~~L~~KSR~~T~~ISV~~D~~ISKNO~~F~~SL~~K~~LN~~N~~StAADI~~Y~~YYC~~A~~R~~G~~I~~V~~Y~~T~~DC~~E~~D~~Y~~W~~G~~Q~~G~~IT~~V~~T~~V~~SS (SEQ ID NO: 46)

CDR1

CDR2

CDR3

47

Figure 18

CTCTCTGTT GCTCCATCAA CAATGGTGTACTACTGGAT TACTACTGGCA GCTGATTCGG CCAGCACCA GGGAAAGGCC TGGAGTGGAT TGGCACATC TATTACAGTG GGACACCTTA
CTACATCCGG TCCCTCAAGA GTCGAACTACCATATCAGTA GACACGCTTA AGAACCGTT CTCCCTGAAG CTGAACTCTG TGACTGCCGC GGACACGGCC GTGTATTACT
GTCGGAGAGG GACAGTAAC~~T~~ ACCTACTACT TGACTACTTG GGGCCAGGGAA ACCCTGGTCA CGCCTCTCTCA (SEQ ID NO: 47)

TTcRASOSIS~~S~~YLNWY~~O~~OKPGKAPKL~~Y~~ASSL~~O~~S~~o~~versrfsgsgsdfltislopedfatyyco~~g~~GYR~~T~~PEPECSF~~Q~~G~~Q~~TKLEKRTV~~A~~PSV~~T~~IFPPSDEQ (SEQ ID NO: 24)

CDR1

CDR2

CDR3

47

Figure 19

ACCATCACTT GCCGGCC~~A~~AG TCAGGAGCATT AGCAGCTAT TAATTCGTA TCAGGAGAA CAGGGAAAG CCCCT AAGCTCTGA TCTATGCTGC ATCCAGTTG
CAAGTGGG TCCC~~A~~TCAG GTCTAGTG GC AGTGGATCTC~~T~~ACCA~~T~~CAG CAGTC~~T~~GC~~A~~ CCTGAAGAT TTGCAACTTA CTACTGCAA
CAGGGTTACA GAACC CCTCCGGAGT GCAGTTGG CCAGGGACC AAGCTGGAGA TCAA (SEQ ID NO: 25)

48

Figure 20

Figure 21

VSGGSVSSgDDxxwswiropgkglewigHLysGNINXNPSLKSRTsLdtsknofslklssvtaadiawyCARDEJGSFEDYwGQGLTVSS (SEQ ID NO:24)

CDR1

CDR2

CDR3

13
49
50

GCTCTGGG GCTCCGTAG CAGTGGTGA TACTACTGG A GCTGGATCCG GCACCCCCA GGGAAAGGGACT TGGAGTGAT TGGACATCTC TATTACAGTG GGAACACCAA
CTACAACCCC TCCCTCAAGA GTCGAGTCAC CATACTCATTA GACACGTCCA AGAACAGTT CTCCCTGAAG CTGAGCTCTG TGACCGCTGC GGACACGGGC GTGTATTACT
GTCGGAGAGA TTTTTGACT GGTTCTCTT TTGACTACTG GGGCCAGGG ACCCTGGTCA CGCTCTCTCA (SEQ ID NO:25)

Figure 23

TTCQASQDISINVNWYOKPGKAPKLINDASDLEIGVPSRISCSGTDFTFISNLOPEDIATYCYCOYDSIPLIFGGTKVEIRRVAAPSVFIFPSDEQ (SEQ ID NO:26)

CDR3

50

14

Figure 24

ACCATCACTT GCCAGGGCAG TCAGGACATA AGCAACTATTAAATTGGTA TCAGCAGAAA CCAGGGAAAG CCCCT AAGCTCTGA TCAACGATGC ATCCGATTG
GAACAGGGG TCCCATCAAG GATAGTGGAA AGTGGATCTG GGACA GATTTACTT TCACCATCAG CAACCTGCAG CCTGAAGATA TTGCAACATA TTACTGTCAA
CAATATGATA (SEQ ID NO:27)

Figure 25

VSGGSVYsgD**Xyywswirroppgkglewignyysgs**TINyNFSLKSRTVSIYDTSKNOFLKLSSVTAA
 CDR1 CDR2 CDR3 (SEQ ID NO:38)



Figure 26

GCTCTGGTG GCTCCGCTTA CAGTGGTGA TACTACTGGA GCTGGATTCG GCAGCCCCCCC GGGAAAGGGAC TGAGGTGGAT TGGTATATC TATTACAGTG GGAGCACCAA
 TACAATCCC TCCTCAAGA GTCGAGTCAC CATATCAGTA GACACGCC AGAACAGCTT CTCCCTGAAG CTGAGCTGC TGACCCCTGC GACACGCC GIGIATTA
 GTCGAGAGA CTCCATACTG GGAGCTACCA ACTACTGGG CCAGGGAAACC CTGGTCACCG TCTCTCA (SEQ ID NO:39)



Figure 27

TTTCQASO**XESNYLXWYQOKPGKAPKXLISD**ASNLEHGPSRFGSGSTXXFTISSLOPEDIATVHCXOYXSPLEGGTVKEIKRTVAAPSVFIFPSDEQ CDR3 (SEQ ID NO:39)

(51)

(52)

Figure 28

ACCATCACTT GCCAGGGAG TCNGGACATT ATAACATT TANATTGTT TCAGCAGAA CCAGGAAAG CCCCT AAMASTCTGA TCTCCGATGC ATCCAATTAA
 GAAACAGGGG TCCCATCGAG GTCTAGTGA AGTGGATCTG GGACA GANTNTACTT TCACCATCGAG CAGGCTGCAG CCTGAAGATA TTGNCACATA TCACTGTCAA
 CAGTATNATA GTCTCCCGCTCACTT TCGGGGAGG GACCAAGTA GAGATCAA (SEQ ID NO:39)

(51)

(52)

Figure 29

vsggvsvssgD_{xw}T_{wro}S_pgkglewigHixsgNNnyneSlksrLrisIdrskIofsLkLssvtaadtaIyycVr_{drytgaed}wgqgtmvtss (SEQ ID NO:3a)

CDR1

CDR2

CDR3

GTCTCTGGTG GTCGCCGTCAG CAGTGGTGTAT TACTACTGGA CCTGGATCCG GCAGCCCCA GCGAAGGGAC TGGAGGTGGAT TGGACACATC TATTACAGTG GGAACACACAA
TTATAACCCC TCCCTCAAGA GTCCGACTCAC CATACTCAATT GACACGTCGA AGACTCAGTT CTCCCTGAGA CTGAGTCTG TGACCCGCTCG GGACACGGCC ATTATTACT;
GTGTGCGAGA TCGAGTCACT GGTGCTTITG ATATCTGGG CCAAGGACA ATGGTCACCG TCCTCTCA (SEQ ID NO:3a)

Figure 31

TTCOASODISNYLNWYOOQPGKAPKL_{LYDASNLEIGVPSRS}SGSGSIDFTISSLOPEDIATFCQHEDHHLPLAFGGGTKEIKRTVAAPSVFIFPSDQE (SEQ ID NO:3b)

CDR1

CDR2

CDR3

17

53

54

Figure 32

ACCATCACTT GCCAGGGCAG TCAGGACATC AGCAACTATT TAAATCCTTA TCAGGAGAAA CCAGGAAAG CCCCT AACACTCTGA TCTACGGATGC ATCCAATTG
GAAACAGGGG TCCCATCAAG GTTCAGTGGAG AGTGGATCTG GGACA GATTACTTCACCAACAG CAGCTGGAG CCTGAAGATA TTGCAACATA TTCTGCAA CACTTGAC
ATCTC CGGCTCCGCTT TCGGGGGAGG GACCAAGGTG GAGATCAA (SEQ ID NO:3c)

18

55

~~CUT & HEAVY~~

E20.1MG30.Seq Sequence

V-DPSO/HU30

DX P4

Fig. 57

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGGATCCAGC	CTTTAGGTC	CATGCCNTTC	TCCCTGTGAG	CGCTCTGGATT	50
A I Q P	F R S	M P F	S C X A	S G F	
CCCCITCAGT	AGNINIGGCA	TGCACITGGT	CCGCCAGGCT	CCAGGCAAGG	100
P F S	X X G M	H W V	R Q A	P G K G	
GGCTGGAGTG	GGTGGCAGTT	ATATGGTATG	ATGGAAGTAA	TAAATACTAT	150
L E W	V A V	I W Y D	G S N	K Y Y	
GCAGACTCCG	TGAAGGGCCG	ATTACACCATIC	TCCAGACACA	ATTCCAAGAA	200
A D S V	K G R	F T I	S R D N	S K N	
CACGCCGTAT	CTGCAAATGA	ACAGACIGAG	AGCCGAGGAC	ACGGCTGIGT	250
T L Y	L Q M N	R L R	A E D	T A V Y	
ATTACIGIGC	CACATTTTC	CACIIC	ACCC	ACAA	300
Y C A	R F L	E W L P	F D Y	W G Q	
CAACGCCAAC	TAACGCCAC	ACCTGCTG	ACTCC	ACCAAGGGCC	350
G T L V	T V X	S D S	T K G P	S V F	
CNCCCTGGGG	CCCTGCTTCC	AGGAGGCACCC	TCNGANAGCA	CANANGGCC	400
X L A	P C F Q	E H P	X X A	X X A P	
CTGGGACTGN	CTGNTACAAG	GACINCITTC	CCTCNAACCN	GGTGACCNIN	450
G T X	X Y K	D X F P	S N X	V T X	
TCNTGGAAA	CICAGNGNC	NICINNATNA	C	(SEQ ID NO: 19)	481
S W E T	Q X X	S X X		(SEQ ID NO: 55)	

20.1 heavy

E20.1VK.Seq Sequence

 $J^k - J^{k3}$

Fig. 58

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGAACCTTIN	GGTCGCNCC	TTTGGAGNC	AGACCCANCA	TCACTTGTCG	50
G T F X	F A P	F G X	R P X I	T C R	
GGCGAGTCAG	GGCATTAGCA	ATTTTTAGC	CIGGTTTCAG	CAGAAACCAG	100
A S Q	G I S N	F L A	W F Q	Q K P G	
GGATAGCCCC	TAAGTCCCTG	ATCTATGCTG	CATCCACITTT	GCCTAAGTGGG	150
I A P	K S L	I Y A A	S T L	Q S G	
GICCCATCAA	AGTTCAACGG	CAGIGGATAT	GGGACACAGTT	TCACTCTCAC	200
V P S K	F T G	S G Y	G T D F	T L T	
CATCAGCAGC	CTGCAGCCTG	AAGACTTTGC	AACTTATTAT	TGICAACAAT	250
I S S	L Q P E	D F A	T Y Y	C Q Q Y	
ATAATGTTA	CCCATTCACT	TTGGGCCCTG	GGACCAAAGT	GGATATCAAA	300
N V Y	P F T	F G P G	T K V	D I K	
CGAACTGTGG	CTGCACCATIC	TGCTCTCATC	TTCCCGCCAT	CTGATGAGCC	350
R T V A	A P S	V F I	F P P S	D E P	
AGTTGAAATC	TGGAACGTGCC	TCTGTGIGT	GCCTGCTGAA	TAACCTCTAT	400
V E I	W N C L	C C V	P A E	. L L S	
CCCAGAGAGG	CCAAAGTACA	GTGGAAGGTG	GATAACGCCN	CNNTTGGCGG	450
Q R G	Q S T	V E G G	.	R X X W R	
NNCCCTTCN	CTCNCCCNIC	CTCNCCCNIC	CTCTCNNA	(SEQID NO:20)489	
X P F X	X P S	S X X	L S X	(SEQID NO:56)	

20.1 Kappa

10	20	30	40	50	
<u>1234567890</u>					50
<u>1234567890</u>					50
AAGCCTGTIG CCTCAGTGCA GGTCCTCIG AAGGCTTCIG GATACACCIT					50
K	P	V	A	S	
S	V	Q	V	S	C
			K	A	S
			S	G	T
				Y	T
				F	
CACCAAGTAT GATACTAACT GGGTGCAGACA GGCCACTGGGA CAAGGGCTTG					100
T	S	Y	D	I	N W V R Q A T G Q G L E
AGTGGATGGG ATGGATGAAC CCTAACAGTG GTAACACAGG CTATGCACAG					150
W M G	W M N	P N S G	N T G	Y A Q	
AAGTCCAGG GCAGAGTCAC CATGACCAGG AACACCTCCA TAAGCACAGC					200
K F Q G	R V T	M T R	N T S I	S T A	
CTACATGGAG CIGAGCAGCC TGAGATCIGA GGACACGGCC GIGIATTACT					250
Y M E	L S S L	R S E	D T A	V Y Y C	
GTGCGAGAGG AGGCCCTAT AGCAGGGCT GGACCTTCIT TGACTACTGG					300
A R G	G P Y	S S G W	T F F	D Y W	
GGCCAGGGAA CCCGGICAC CGTCCTCCA GCGCTNCACC AAGGGCCCAT					350
G Q G T	L V T	V S S	A L H Q	G P I	
CGGCTTCCC CCTGGAGGCC TGCTCCAGGA GCACCTCCCA GAGCACANIC					400
G L P	P G A L	L Q E	H L P	E H X X	
NNCCCTGGG CTGCCTGGNN CAAGGACTCT TTCCCCAAC CCCGGNTGA					449 (SEQ ID NO:21)
P L G	C L X	Q G L F	P X T	P X	(SEQ ID NO:57)

DNI

20.3 heavy

Lent 20.3 Kappa

E20.3VK.Seq Sequence

JK- JK⁴

Fig. 60

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TTTGAACCT	TCTGGCGT	GTCCTGGC	GGAGGGCA	CCATCACTG	50
F E P F	X A V S	L G A R A T	I N C		
CAAGTCCAGC	CAGCGTGTT	TATACTTC	CAACAATAAG	AACTGCCTAG	100
K S S Q	R V L Y X S	N N K N C L A			
CTTGGTACCA	GCAGAAACCA	GGACAGCCTC	CTAAGCTGCT	CATTACTGG	150
W Y Q Q	K P G Q P P	K L L I Y W			
ACATCTACCC	GGGAATCCGG	GGTCCCTGCC	CGATTCACTG	GCAGGGTC	200
T S T R E S G V P A	R F S G S G S				
TGGGACAGAT	TTCACCTCTCA	CCATCAGCAG	CTCTGAGGCT	GAAGATGIGG	250
G T D F T L T I S S	L Q A E D V A				
CAGTTTATTA	CTGTCAAA	TATTATAGTA	CTCCACTCAC	TTTCGGCGGA	300
V Y Y C Q Q Y Y S T	P L T F G G				
GGGACCATGG	TGGAGATCAA	GGAACTGIG	GCTGCACCAT	CTGCTCTCAT	350
G T M V E I K R T V	A A P S V F I				
CTTCCCGCCA	TCTGATGAGC	CNGTNTGAAA	TCTGGAACTG	CCTCTGTTTG	400
F P P S D E P V . N	L E L P L F V				
TGTGCCCCGC	TGAATAACTT	CTATCCCAGA	GAGGCCAAAG	TACCACTGGA	450
C P A E . L	L S Q R G Q S T S G				
AGGTTGATAA	(SEQ ID NO: 22)				460
R W I	(SEQ ID NO: 58)				

20.3 Kappa

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CNGCCTGTTA	GGTCCNTGCG	ACTCCTCTGT	GCAGCGCTTG	GATTCACTT	50
X P V R	S X R	L S C	A A S G	F I F	
CAGTAGNTAT	GGCATGCCACT	GGGTCCGCCA	GGCTCCAGGC	AAGGGGCTGG	100
S X Y	G M H W	V R Q	A P G	K G L E	
AGIGGGTGGC	AATTATATGG	TATGATGGAA	GTAATAAATA	CTATGCAGAC	150
W V A	I I W	Y D G S	N K Y	Y A D	
TCCGIGAAGG	GGCGATTACAC	CATCTCCAGA	GACAATTCCA	AGAACACCGT	200
S V K G	R F T	I S R	D N S K	N T L	
GTATCTGCAA	ATGAACAGOC	TGAGAGCCGA	GGACACGGCT	GIGTATTACT	250
Y L Q	M N S L	R A E	D T A	V Y Y C	
GTGCGAGAGA	CGGGGGGCCA	<u>CGGTGGTTTC</u>	TOGCTCTCTGA	CTACTGGGGC	300
A R D	G G P	R W F L	A S D	Y W G	
CAGGGAACCC	TGGTCACCGT	CICCTCAGCC	TCCACCAAGG	GCCCCATGGT	350
Q G T L	V T V	S S A	S T K G	P S V	
CTTCCCCCTG	GGCCCTGCT	CCAGGAGCAC	CCCTCAGAGAG	CACAGCGGCC	400
F P L	A P C S	R S T	L R E	H S G P	
CTGGGCTGCC	TGGTCAAGG	ACTACTTCC	CGGAACCGGT	GACGGTGTNC	450
G L P	G S R	T T F P	E P V	T V X	
GTGGAACTC ATGAC	(SEQ ID NO: 23)				465
V G T H D	(SEQ ID NO: 59)				

20.8.1 (copy)

E20.8.1MG18.Seq Sequence

JK- JK2

Fig. 62

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
AGTCTCCAGA	CICCCCTGGT	GIGCTCTGG	GCGAGAGGGC	CACCATCAAC	50
S L Q T	P W L	C L W	A R G P	P S T	
TGCAAGTC	CA GNCAGAGTAT	TTTATACAGC	TCCAACAATC	AAAAACTTCT	100
A S P	X R V F	Y T A	P T I	K N F L	
TAGCTTGGTA	CCAGCAGAAA	CCAGGACAGC	CTCCGAAGTT	GCTCATTTAC	150
A W Y	Q Q K	P G Q P	P K L	L I Y	
TGGGCATCTA	TTGGGAATC	CGGGGTCCCT	GACCGATTCA	GIGGCAGCGG	200
W A S I	R E S	G V P	D R F S	G S G	
GCTGGGACA	GATTCACTC	TCACCATCAG	CAGCTTGCAG	GCIGAAGATG	250
S G T	D F T L	T I S	S L Q	A E D V	
TGGCAGTTA	TTACIGICAG	CAGTATTATA	GTATCCGIG	CACTTTGGC	300
A V Y	Y C Q	Q Y Y S	I P C	T F G	
CAGGGGACCA	AGCTGGAGAT	CAAACGAACT	GIGGCTGCAC	CATCTGCTT	350
Q G T K	L E I	K R T	V A A P	S V F	
CATCTTCCCCG	CCATCTGATG	AGCAGITGAA	ATCTGGAACT	GCCTCTGTTG	400
I F P	P S D E	Q L K	S G T	A S V V	
TGIGCCTGCT	GAATAACTTC	TATCCCAGAA	AGGCCAAAGT	ACATGAAGGG	450
C L L	N N F	Y P R K	A K V	H E G	
TICAAA	(SEQ ID NO: 24)				456
F K	(SEQ ID NO: 60)				

20.81 kappa

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
GGCGTGGYCC	AGCCTGKGAG	GTCCCTGAGA	CCTCTCTGTG	CAGCGCTG	50
G V X Q	P X R	S L R	L S C A	A S G	
ATTCACTTC	AGTARCTATG	GCATGCACTG	GGTCGCCAG	GCTCCAGGCA	100
F X F	S X Y G	M H W	V R Q	A P G K	
AGGGGCTGGA	GTGGGTGGCA	ATTATAATGGT	ATGATGGAAG	TAGCAAATAC	150
G L E	W V A	I I W Y	D G S	S K Y	
TATGCCAGACT	CCGIGAAGGG	CCGATTICACC	ATCTCAGAG	ACAATTCCAA	200
Y A D S	V K G	R F T	I S R D	N S K	
GAACACGCTG	TATCTGCAAA	TGAACAGCCT	GAGAGCCAG	GACACGGCTG	250
N T L	Y L Q M	N S L	R A E	D T A V	
TGTATTACTG	TGCGAGAGAC	GGGGGGCAC	GGTGGTTCT	CGCTTCGAC	300
Y Y C	A R D	G G P R	W F L	A S D	
TACTGGGCC	AGGAAACCT	GGTCACCGTC	TCCTCAGCCT	CCACCAAGGG	350
Y W G Q	G T L	V T V	S S A S	T K G	
CCCATCGGT	TTCCCCCTGG	CGCCCTGCTC	CAGGAGCACC	TTCCGAGAGC	400
P S V	F P L A	P C S	R S T	F R E H	
ACAGCGGCC	TGGCTGCCT	GGTCAAGGAC	TACTCCCCG	AAMCGGTGAC	450
S G P	G L P	G Q G L	L P R	X G D	
GGTGTCGIGG	AACTCAGGCG	CCTCTGACCAG	NGGCGIGCAC	AATTCCCAGC	500
G V V E	L R R	S D Q	X R A Q	F P A	
NGICCINAAG	GTGAAATCG	TAANGTTCA AA	(SEQ ID NO: 25)		532
V L K	V E I V	X V Q	(SEQ ID NO: 61)		

20.11.2. heavy

10	20	30	40	50	
<u>1234567890</u>					50
ACTCAGTCTC CAGACTCCCT GGCTGIGCT CTGGGGAGA GGGCCACCAT					50
T	Q	S	P	D S L A V S L G E R A T I	
CAACTGCAAG TCCAGCCAGA GIGTTTATA CGGCTCCAAG AATCAGAACT					100
N	C	K	S S Q S	V L Y G S K N Q N Y	
ACTTAGCTTG GTACCAGCAG AAACCAGGAC AGCCTCCCAA GCTGCTCATT					150
L	A	W	Y Q Q	K P G Q P P K L L I	
TACTGGGCAT CTACCCGGGA ATCCGGGTG CCTGACOGAT TCAGGGGCAG					200
Y	W	A	S T R E	S G V P D R F R G S	
CGGGCTAGG ACAGATTICA CTCACCAT CAGCAGCTG CAGGCIGAAG					250
G	S	R	T D F T	L T I S S L Q A E D	
ATGIGGCAGT TTACTTCIGT CACCAATAATT ATAGTACTCC GTGGACGGTC					300
V	A	V	Y F C H Q Y Y	S T P W T F	
GGCCAAGGGA CCAAGGTGGA AATCAAACGA ACTGIGGCTG CACCATCTG					350
G	Q	G	T K V E	I K R T V A A P S V	
CTTCATCTTC CGGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCCTG					400
F	I	F	P P S D	E Q L K S G T A S V	
TIGIGIGCCT GCTGAATAAC TIGIATCCCA GAAAGCCAAG GACACGAAAG					450
V	C	L	L N N	L Y P R K P R T R K	
GTCANACCCA CCC (SEQ ID NO: 26)					463
V	X	P	T	(SEQ ID NO: 62)	

20.11.2 Kappa

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CGIGATCCNC	CTGGNTGGTC	CCTGAGACTC	TCCTGIGCAG	CGTCTGGATT	50
R D P P	G W S	L R L	S C A A	S G F	
CATCTTCANT	AACTATINCA	TGCAC TGGGT	CCGCCAGGCT	CCAGGCAAGG	100
I F X	N Y X M	H W V	R Q A	P G K G	
GGCTGGAGTG	GGTGGCAATT	ATATGGTATG	ATGGAAGTAG	CAAATACTAT	150
L E W	V A I	I W Y D	G S S	K Y Y	
GCAGACTCCG	NGAAGGGCCG	ATTCACCATC	TCCAGAGACA	ATTCCAAGAA	200
A D S X	K G R	F T I	S R D N	S K N	
CACCGCTGAT	CIGCAAATGA	ACAGCCTGAG	AGCCGAGGAC	ACGGCIGATG	250
T L Y	L Q M N	S L R	A E D	T A D V	
TATTACTGIG	CGAGAGACGG	TIGGCCACG	GTGGCTTCCTC	GCTTCTGACT	300
L L C	E R R	L G H G	G F S	L L T	
ACTGGNGCNC	AGGGCAACNC	TGN CINACCG	TNTTCCTCAN	CCCINACNC	350
T G A Q	G N X	X X P	X S S X	L Y X	
AAGGGCCNCC	ATINGGICCTT	TCCCCCCTGG	NNNNCTGCT	CNATGNINCA	400
R A X	I X S F	P P G	X P A	X X X T	
CCCTINCACAC	NONACAN	(SEQ ID NO: 27)			417
L R X	X X	(SEQ ID NO: 63)			

2018 heavy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
TTCGIGGCTG	TGCTCTTGG	CGAGAGGNCC	ACCATCAACT	GCAAGTCCAG	50
F V A V	S L G	E R X	T I N C	K S S	
CCAGAGTATT	TTATACAGCT	CCAACAATCA	AAACTTCTTA	GCTTGGTACC	100
Q S I	L Y S S	N N Q	N F L	A W Y Q	
AGCAGAAACC	AGGACAGCCT	CCGAAGTTGC	TCATTTACTG	GGCATCTAATT	150
Q K P	G Q P	P K L L	I Y W	A S I	
CGGGAATCCG	GGGTCCCCGTA	CGGATTCACTG	GGCAGCGGGT	CTGGGACAGA	200
R E S G	V P D	R F S	G S G S	G T D	
TTTCACTCTC	ACCATCAGCA	GGCTGCCAGGC	TGAAGATGIG	GCAGTTTATT	250
F T L	T I S S	L Q A	E D V	A V Y Y	
ACTGTCAGCA	GTATTATAGT	ATTCGGTGCA	CTTTTGGCCA	GGGGACCAAG	300
C Q Q	Y Y S	I P C T	F G Q	G T K	
CTGGAGATCA	AACGAACGTG	GGCTGCACCA	TCTGCTCTCA	TCTTCCCGGCC	350
L E I K	R T V	A A P	S V F I	F P P	
ATCTGATGAG	CCAAGNTTGA	AAATCTGGAA	CTGCCCTCTGT	TGTGIGGCCCT	400
S D E	P X L K	I W N	C L C	C V P C	
GCTTGAATAA	CTCTATCCC	AGAGANGGCC	AAAGTCCTGT	GGAGGTGGA	450
L N N	F Y P	R X G Q	S P V	E G G	
TAC	(SEQ ID NO: 28)				453
Y	(SEQ ID NO: 64)				

20.18 Kappa

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTCACCTGCA	CTGCTCTGG	TGGCTCCATC	AGTAGTTACT	NTGGAGNTG	50
L T C T	V S G	G S I	S S Y X	W X W	
GATCGGGCAG CCCGNAGGGA AGGGACTGGA GIGGATGGG TGTTTCTATT					100
I R Q	P X G K	G L E	W I G	C F Y Y	
ACAGNGGGAG CACCAACTAC AACCCCTCCC TNAAGAGTCA TGTCAACCATA					150
X G S	T N Y	N P S L	K S H	V T I	
TCAGTAGACA CGTCCAAGAA CCAGTTCTAC NTGAAGCTGA GCINTGIGAC					200
S V D T	S K N	Q F Y	X K L S	X V T	
CGNTGGGAC ACGNCNGA ATAACGTNGC NAGAGATAGG GGAGNAGIGN					250
X A D	T X X N	N X A	R D R	G X V X	
NNIGGCNINC	TACINTGACT	ACTGAGGCCA	GNGAACNTG	GNTCACAGTA	300
W X X	T X T	T E A X	E P W	X T V	
ATCCNTAAGN	CINCAANCA	AANGNGNCCC	AANGNGANAC	NINNCINCN	350 (SEQ ID NO: 29)
I X K X	X X Q	X X P	X X X X	X X	(SEQ ID NO: 65)

W.19.2 heavy

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	50
TCTTGGTAG CGNGCTTGG CGAGAGGCC ACCATCACT GCAAGTCCAG					50
S L V A X L G E R P T I N C K S S					
CCAGAGTGTT TTATACNGCT CCAAGAATCA GAACTACTTA GCTTGGTACC					100
Q S V L Y X S K N Q N Y L A W Y Q					
AGCAGAAACC AGGACAGCCT CCTAAGCTGC TCATTACTG GGCACTCTACC					150
Q K P G Q P P K L L I Y W A S T					
CGGGAATCGG GGGTCCCTGA CGGATTCAAGG CCCAGGGGT CTAGGACAGA					200
R E S G V P D R F R G S G S R T D					
TTCACITCTC ACCATCAGCA GCCTGGAGGC TGAACATGIG GCAGTTACT					250
F T L T I S S L Q A E D V A V Y F					
TCTGICACCA ATATTATAGT ACTCCGIGGA CGTTCGGCCA AGGGACCAAG					300
C H Q Y Y S T P W T F G Q G T K					
GIGGAAATCA AACGAACGT GGCTGCACCA TCTGICCTCA TCTTCCCGCC					350
V E I K R T V A A P S V F I F P P					
ATCTGATGAG CACCTTGAAA TCTCTGAACT GCCTCTGNTG NGTGCCTGCT					400
S D E H L E I L E L P L X X A C .					
GAACNAACTC TATCCCCAGA GANGGCCAA AAGINTCAAG NNGNNAGGC					450
T N S I P R X G P K V S X X X G					
NNGATAACGC CINTCNCON NCNINC (SEQ ID NO: 30)					476
X I T P X X X X (SEQ ID NO: 66)					

20.19.2 Kappa

E6Fr 20.21 Heavy

20.20.21MG30.Seq Sequence

V-DP6S
D DIR3
J-JH6b

69

Fig. 69

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
AAGCCTTTC	AGACCNIGCC	CITCACCTGC	ACTGCTCTG	GIGGCTCCAT	50
K P F Q	T X P	F T C	T V S G	G S I	
CAGCAGTGTT	GGTTACTACT	GGAGCTGGAT	CGGCCAGCAC	CCAGGGAAAGG	100
S S G	G Y Y W	S W I	R Q H	P G K G	
GCTGGAGTGT	GATTGGGTAC	ATCTATAACA	GIGGGAGCAC	CTACTACAAAC	150
L E W	I G Y	I Y N S	G S T	Y Y N	
CCGCCCCCTCC	ACAGTCGAGT	TACCATATCA	GTAGACACGT	CTAAGAACCA	200
P S L Q	S R V	T I S	V D T S	K N Q	
GTCTCCCTTG	AAGCTGAGCT	CIGGACTGTC	CCGGACACCG	GCGGTTATT	250
F S L	K L S S	V T A	A D T	A V Y Y	
ACTGTGCGGG	<u>TCAGAAATGG</u>	TCCTACTACT	ACTACTACGG	TATGGACGTC	300
C A G	Q K W	S Y Y Y	Y Y G	M D V	
TGGGGCCAAG	GGACCACGGT	CACCGTCTCC	TNAGCCTCCA	CCAANGGCC	350
W G Q G	T T V	T V S	X A S T	X G P	
ATCGGCTTC	CCCTGGCGC	CCTGNCTTAG	GAGCACCTCC	CANAGCACAG	400
S V F	P L A P	X S R	S T S	X S T D	
ACGGATNCIG	GGCTTGCTTG	NATCAATGGA	CTACTTCCC	CGAACCGGIT	450
G X W	A C L	X Q W T	T F P	E P V	
GNNIGIGNNN	CCTGGNAACT N	(SEQ ID NO: 31)			471
X C X X	W X L	(SEQ ID NO: 67)			

20.21 heavy

t6tr t 20.22 heavy

20.22MG30.Seq Sequence

D-D1R4
J-JH66

70

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
AAGCCTTNG	AGACCNFGCC	CCTCACCTGCG	ACTGTCCTG	GIGGCTCCAT	50
K P X E	T X P L T C	T V S G	G S I		
CAGTAATTAC	TACTGGAGCT	GGATCCGGCA	GCCCCCAGGG	AAGGGACTGG	100
S N Y	Y W S W	I R Q	P P G	K G L E	
AGTGGATTGG	GTATACTAT	TACAGTGGGA	GCACCAACTA	CAACCCCTCC	150
W I G	Y I Y	Y S G S	T N Y	N P S	
CTCAAGAGIC	GAGICACCAT	ATCAGTAGAC	ACGTCCAAGA	ACCAGTTC	200
L K S R	V T I	S V D	T S K N	Q F S	
CCIGAAGCTG	AGCCTGIGA	CGCGTGGGA	CAOGGCGGIG	TATTACTGIG	250
L K L	S S V T	A A D	T A V	Y Y C A	
CGAGACGGCC	CGGGGGGAGC	TACTACTACT	ACGGTATGGA	CGCTGGGCC	300
R G P	G G , S	Y Y Y Y	G M D	V W G	
CAAGGGACCA	CGGTCACCGT	CTCCCTAGCC	TCCACCAAGG	GCCCCATGGT	350
Q G T T	V T V	S S A	S T K G	P S V	
CTTCCCCCTG	GGGCCCCCTGCT	CCAGGAGCAC	CTCCGAGAGC	ACAGCGGCC	400
F P L	A P C S	R S T	S E S	T A A L	
TGGGCTGCCT	GGGICAAGGA	CTACTTCCCC	GAACCGGIGA	CGGTGTTGN	450
G C L	G Q G	L L P R	T G D	G V R	
NGGAAC	(SEQ ID NO: 32)				456
X N	(SEQ ID NO: 68)				

Fig. 70

20.22 heavy

E7.5.2.K.aa Sequence

Figure 72

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTGTCIGCAT	CTGTAGGAGA	CAGAGTCATA	ATCACTTGCC	GGGCAAGTCA	50
L S A S	V G D	R V I	I T C R	A S Q	
AAACATCACC	GACCATTAA	ATIGGIATCA	GCAGATAGCA	GGAAAAGCCC	100
N I T	D H L N	W Y Q	Q I A	G K A P	
CTAGGCCCT	GATATACACT	GCATCCAGTT	TGCAAGGTGG	GGTCCCCATCA	150
R P L	I Y T	A S S L	Q G G	V P S	
AGGTCAGTG	GCAGTGGATC	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	200
R F S G	S G S	G T D	F T L T	I S S	
TCTGCAACCT	GAAGATTTTT	CAACTTACTA	CTGTCAACAG	AGITACAGTA	250
L Q P	E D F S	T Y Y	C Q Q	S Y S T	
CCCCGTGCAG	TTTGGCCAG	GGGACCAAGC	TGGAGATCAA	ACGAACTGTG	300
P C S	F G Q	G T K L	E I K	R T V	
GCTGCACCAT	CTGICCTCAT	CITCCCGCCA	TCTGATGAGC	AGITGAAATC	350
A A P S	V F I	F P P	S D E Q	L K S	
TGGAACIGCC	TCTGTTGTGT	GCCTGCTGAA	TAACCTCTAT	CCCA	394 (SEQ ID NO: 33)
G T A S	V V C	L L N	N F Y	P	(SEQ ID NO: 69)

7.5.2 heavy

E7.5.2.v.aa Sequence

Figure 73

10	20	30	40	50	
<u>1234567890</u>	<u>1234567890</u>	<u>1234567890</u>	<u>1234567890</u>	<u>1234567890</u>	
G T G A A G G I C T	C C T G C A A G G C	T T C T G G A T A C	A C C T T C A G C G	G C T A C T A T A T	50
V K V S	C K A	S G Y	T F S G	Y Y M	
G C A C T G G G T G	C G A C A G G C C C	C T G G A C A A G G	G C T T G A G T G G	A T G G G A T C G A	100
H W V	R Q A P	G Q G	L E W	M G S I	
T C C A C C T A A	C A G I G G I G G C	A N A A C T T T G	C A C A G A A G I T	T C A G G G C A G G	150
H P N	S G G	X N F A	Q K F	Q G R	
G T C A C C A T G A	C C A G G G A C A C	G T C C A T C A A C	A C A G G C T A C T	T G G A G G T G A G	200
V T M T	R D T	S I N	T A Y L	E L S	
C A G G C T G A G A	T C T G A C G A C A	C G G C C G T G T A	T T A C T G T G C G	A G A G A T A A A A	250
R L R	S D D T	A V Y	Y C A	R D K N	
A C T A C G G I G A	C T A C G I C T T T	G A C T A T T G G G	G C C A G G G A A C	C C T G G G I C A C C	300
Y G D	Y V F	D Y W G	Q G T	L V T	
G T C T C C T C A G	(SEQ ID NO: 34)				310
V S S	(SEQ ID NO: 70)				

75.2Kppm